

## Online resource 3

### **Global epigenetic profiling identifies methylation subgroups associated with recurrence-free survival in meningioma**

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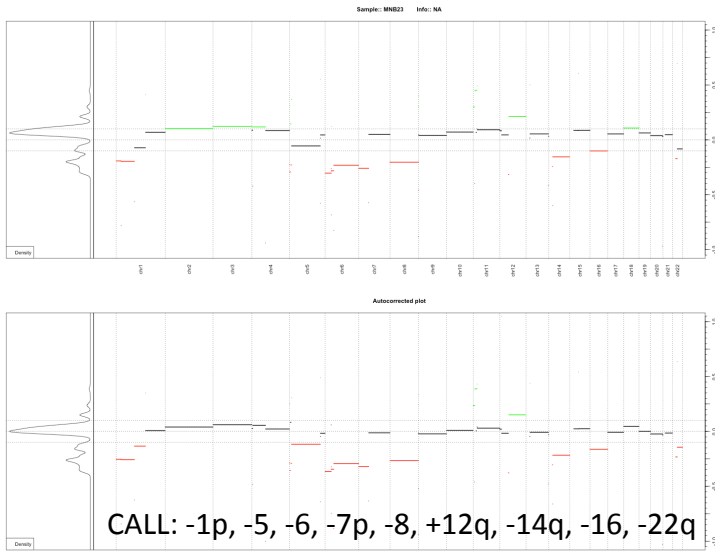
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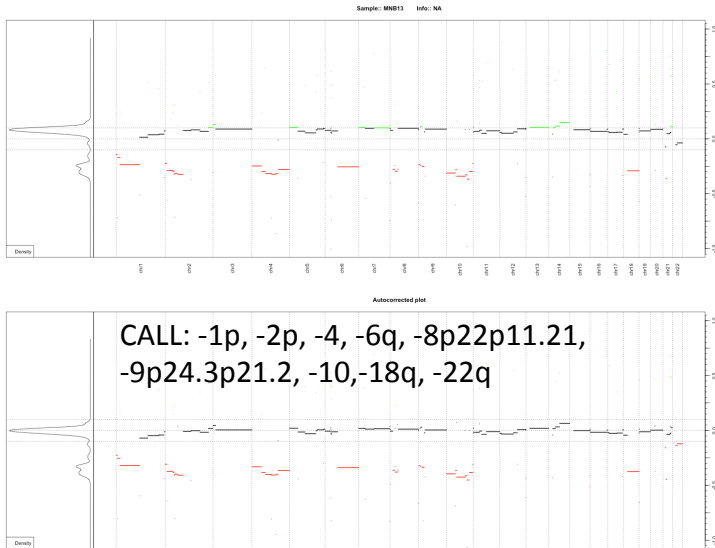
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# Copy number baseline correction and calling

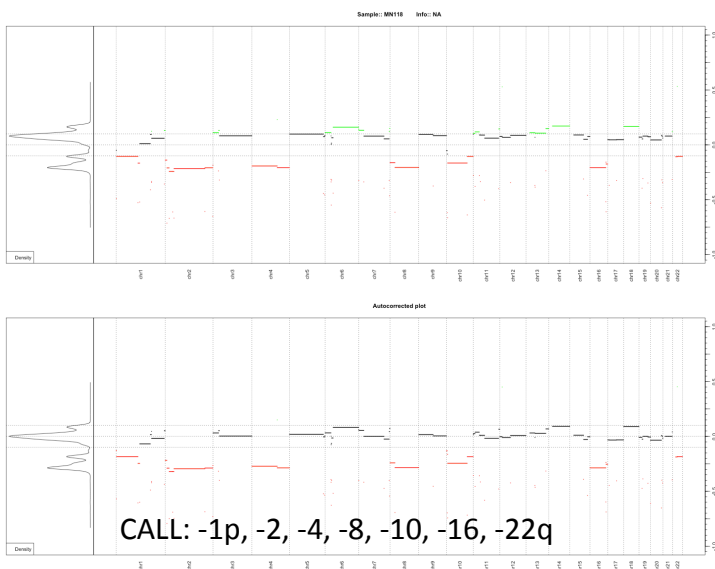
**A**



**B**



**C**



Copy number aberration (CNA) information was extracted from the 450k methylation data (intensity values) using the CopyNumber450k Cancer R package. Because of the frequent false sample centering and baseline shifting, CNA calling in cancer samples is frequently problematic. This package was designed to correct the baseline in cancer samples using the maximum density peak estimation (MDPE) method [1]. Briefly the correction is made by shifting the sample log values in an amount equal to the difference between the sample baseline and the maximum peak level.

The minimum number of probes required for plotting was 3. The cutoff was 0.1. Following correction all samples were reviewed manually. For partial/segmental calls information was retrieved from Integrative Genomics Viewer (IGV) v. 2.3.68 (97) (hg19).

A few examples are shown here (A, B, C) where the autocorrection implemented had an impact on the final CNA call.

## Reference:

[1] Marzouka NA, Nordlund J, Backlin CL, Lonnerholm G, Syvanen AC, Carlsson Almlof J (2016)

CopyNumber450kCancer: baseline correction for accurate copy number calling from the 450k methylation array. *Bioinformatics* 32:1080-1082. doi:10.1093/bioinformatics/btv652